

SEQUENCE LISTING

<110> Duvick, Jonathan P.  
Gilliam, Jacob T.  
Maddox, Joyce R.  
Crasta, Oswald R.  
Folkerts, Otto

<120> Amino Polyol Amine Oxidase  
Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<140> 09/770,564  
<141> 2001-01-26

<150> US 60/092,936  
<151> 1998-07-15

<150> US 09/352,168  
<151> 1999-07-12

<160> 35

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatacg gatggggtca cagctcgatt 180  
ggaggacgccc cgagaagcct tggcgccacc accacggctt gtcccataacg aagactatct 240  
tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg 300  
gtaaaaatgt caaggtggaa tacaaggatgg 360  
gtggtaacga aaccancacc ttttgcttc 372  
ggaacacggc gc

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tacaaggatgg tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccggacc 120

gatcgtaactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgagggtgc 180  
 ac 182

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 <213> Artificial Sequence

<220>  
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<400> 3  
 tggtttcgtt accgacaacc ttgtatccc 29

<210> 4  
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 <212> DNA  
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<220>  
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 gagtttgtcc cagacagact tttgtcgt 28

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 1 5 10 15

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96  
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
 20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct ggc tgg atc aat gac 192  
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp

85	90	95	
ggt aca acc act aca gct tat ggt gac tcc ttg ctg agc gag gag Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu 100	105	110	336
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile 115	120	125	384
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cg Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg 130	135	140	432
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145	150	155	480
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165	170	175	528
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180	185	190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195	200	205	624
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210	215	220	672
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225	230	235	720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245	250	255	768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu 260	265	270	816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275	280	285	864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290	295	300	912
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln 305	310	315	960

tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc		1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val		
325	330	335
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg		1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg		
340	345	350
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac		1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp		
355	360	365
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg		1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro		
370	375	380
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga		1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly		
385	390	395
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg		1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser		
405	410	415
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg		1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr		
420	425	430
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa		1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln		
435	440	445
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca		1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
450	455	460
tag		1389
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<211> 462		
<212> PRT		
<213> Exophiala spinifera		
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20 25 30		
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly		
35 40 45		
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp		
50 55 60		
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu		
65 70 75 80		
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp		
85 90 95		

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
     100                105                        110  
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
     115                120                        125  
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
     130                135                        140  
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
     145                150                        155                        160  
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
     165                170                        175  
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
     180                185                        190  
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
     195                200                        205  
 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
     210                215                        220  
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
     225                230                        235                        240  
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
     245                250                        255  
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu  
     260                265                        270  
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
     275                280                        285  
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
     290                295                        300  
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
     305                310                        315                        320  
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
     325                330                        335  
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
     340                345                        350  
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
     355                360                        365  
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
     370                375                        380  
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
     385                390                        395                        400  
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
     405                410                        415  
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
     420                425                        430  
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
     435                440                        445  
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
     450                455                        460

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<221> intron

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96  
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336  
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480  
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt 528  
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag 576  
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg 624  
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly

195	200	205	
cag tat gtg cga tgc aaa aca g	gtgcgtgtgg	tgtcgctcta	ggtgaaaaac
Gln Tyr Val Arg Cys Lys Thr			676
210	215		
tcgtttctca gtggcattc cag gt atg cag tcg att tgc cat gcc atg tca			728
Gly Met Gln Ser Ile Cys His Ala Met Ser			
220	225		
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa			776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu			
230	235	240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc			824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala			
245	250	255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat			872
Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr			
260	265	270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg			920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu			
275	280	285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg			968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			
290	295	300	305
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg			1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			
310	315	320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat			1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
325	330	335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag			1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
340	345	350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
355	360	365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
370	375	380	385
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
390	395	400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
405	410	415	

ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct 1352  
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser  
420 425 430

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga 1400  
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
435 440 445

ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1442  
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

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<211> 462  
<212> PRT  
<213> Exophiala spinifera

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95  
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140  
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160  
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175  
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190  
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205  
Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
210 215 220  
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
225 230 235 240  
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
245 250 255  
Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu  
260 265 270  
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
275 280 285  
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val

290	295	300
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln		
305	310	315 320
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val		
325	330	335
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg		
340	345	350
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp		
355	360	365
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro		
370	375	380
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly		
385	390	395 400
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser		
405	410	415
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr		
420	425	430
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln		
435	440	445
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
450	455	460

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<212> PRT  
<213> Exophiala spinifera

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly		
35	40	45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp		
50	55	60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu		
65	70	75 80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp		
85	90	95
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu		
100	105	110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile		
115	120	125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg		
130	135	140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu		
145	150	155 160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		
165	170	175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
180	185	190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
195	200	205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly		
210	215	220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met  
 225 230 235 240  
 Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro  
 245 250 255  
 Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro  
 260 265 270  
 Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln  
 275 280 285  
 Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys  
 290 295 300  
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr  
 305 310 315 320  
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn  
 325 330 335  
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser  
 340 345 350  
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly  
 355 360 365  
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr  
 370 375 380  
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg  
 385 390 395 400  
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu  
 405 410 415  
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg  
 420 425 430  
 Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu  
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 450 455

<210> 10  
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<220>  
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 <222> (1)...(1389)

<221> misc\_feature  
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 <223> Extra lysine in K:trAPAO

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 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30  
  
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50	55
55	60
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65	70
75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85	90
90	95
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100	105
105	110
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115	120
120	125
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130	135
135	140
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145	150
150	155
155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165	170
170	175
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180	185
185	190
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195	200
200	205
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210	215
215	220
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225	230
230	235
235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245	250
250	255
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260	265
265	270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa		864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln		
275	280	285
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
290	295	300
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
305	310	315
320		
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac		1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
325	330	335
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
340	345	350
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
355	360	365
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
370	375	380
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa		1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
385	390	395
400		
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt		1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly		
405	410	415
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag		1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu		
420	425	430
435		
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt		1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
440	445	
450	455	460
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca		1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
450	455	460
tag		1392
<210> 11		
<211> 463		
<212> PRT		
<213> Exophiala spinifera		
<220>		
<221> VARIANT		

<222> (1)...(1)

<223> Extra lysine in the polypeptide sequence of  
K:trAPAO.

<400> 11

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30  
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45  
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60  
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80  
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95  
Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110  
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125  
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140  
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160  
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175  
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190  
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205  
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
210 215 220  
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240  
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255  
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270  
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285  
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300  
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320  
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335  
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350  
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365  
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380  
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400  
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly

	405	410	415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 12  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer sequence designed for cloning DNA into  
expression vectors, N23256

<400> 12  
gggaaattca aagacaacgt tgccggacgtg gtag 34

<210> 13  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer sequence designed for cloning DNA into  
expression vectors, N23259

<400> 13  
ggggcggccg cctatgctgc tggcaccagg ctag 34

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14  
tggtttcgtt accgacaacc ttgtatccc 29

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide for 5' race, N21968

<400> 15  
gagttgggcc cagacagact tttgtcg 28

<210> 16

<211> 1673  
 <212> DNA  
 <213> Exophiala spinifera  
  
 <220>  
 <221> sig\_peptide  
 <222> (1)...(267)  
 <223> yeast alpha mating factor secretion signal  
  
 <221> CDS  
 <222> (1)...(1662)  
  
 <400> 16

atg	aga	ttt	cct	tca	att	ttt	act	gct	gtt	tta	ttc	gca	gca	tcc	tcc	48
Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser	
															-75	
															-85	
															-80	

  

gca	tta	gct	gct	cca	gtc	aac	act	aca	aca	gaa	gat	gaa	acg	gca	caa	96
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln		
															-60	
															-70	
															-65	

  

att	ccg	gct	gaa	gct	gtc	atc	ggt	tac	tca	gat	tta	gaa	ggg	gat	ttc	144
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
															-45	
															-50	

  

gat	gtt	gct	gtt	ttg	cca	ttt	tcc	aac	agc	aca	aat	aac	ggg	tta	ttg	192
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
															-30	
															-40	

  

ttt	ata	aat	act	act	att	gcc	agc	att	gct	gct	aaa	gaa	gaa	ggg	gta	240
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
															-10	
															-25	
															-20	

  

tct	ctc	gag	aaa	aga	gag	gct	gaa	gct	gaa	ttc	aaa	gac	aac	gtt	gcg	288
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala	
															5	
															-5	

  

gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	336
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	
															10	
															15	

  

aaa	gtc	cag	gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gct	atg	gat	384
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	
															25	
															30	

  

cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	432
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	
															40	
															45	

  

act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	480
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	
															60	
															65	

  

gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	528
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	
															75	
															80	

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act	576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca	624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc	672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg	720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc	768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	
155 160 165	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac	816
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185 190 195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200 205 210 215	
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
220 225 230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
235 240 245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
250 255 260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
265 270 275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
280 285 290 295	
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
300 305 310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac	1248

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
315	320	325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
330	335	340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
345	350	355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
360	365	370	375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
380	385	390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
395	400	405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
410	415	420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
425	430	435	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca			1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala			
440	445	450	455
gaa gtt gtg gct agc ctg gtg cca gca gca taggcccccc c			1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala			
460	465		

<210> 17  
<211> 554  
<212> PRT  
<213> Exophiala spinifera

<220>  
<221> SIGNAL  
<222> (1)...(89)  
<223> yeast alpha mating factor secretion signal

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-85 -80 -75  
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
-70 -65 -60  
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
-55 -50 -45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
     -40                  -35                  -30  
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
     -25                  -20                  -15                  -10  
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala  
     -5                  1                  5  
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg  
     10                  15                  20  
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp  
     25                  30                  35  
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr  
     40                  45                  50                  55  
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser  
     60                  65                  70  
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln  
     75                  80                  85  
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr  
     90                  95                  100  
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala  
     105                 110                 115  
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser  
     120                 125                 130                 135  
 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val  
     140                 145                 150  
 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu  
     155                 160                 165  
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His  
     170                 175                 180  
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly  
     185                 190                 195  
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg  
     200                 205                 210                 215  
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu  
     220                 225                 230  
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln  
     235                 240                 245  
 Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg  
     250                 255                 260  
 Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu  
     265                 270                 275  
 Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn  
     280                 285                 290                 295  
 Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro  
     300                 305                 310  
 Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp  
     315                 320                 325  
 Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp  
     330                 335                 340  
 Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln  
     345                 350                 355  
 Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala  
     360                 365                 370                 375  
 Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu  
     380                 385                 390  
 Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala  
     395                 400                 405  
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr

410	415	420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp		
425	430	435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala		
440	445	450
Glu Val Val Ala Ser Leu Val Pro Ala Ala		455
460	465	

<210> 18  
<211> 2079  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)...(2076)  
<223>

<221> misc\_feature  
<222> (1)...(687)  
<223> gst fusion + polylinker

<221> misc\_feature  
<222> (688)...(2076)  
<223> K:trAPAO

<221> misc\_feature  
<222> (688)...(690)  
<223> Extra lysine

<223> GST:K:trAPAO fusion for bacterial expression.

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atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
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1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
																85
																90
																95
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt															336	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
																100
																105
																110
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa															384	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
																115
																120
																125
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat															432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
																130
																135
																140
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat															480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
																145
																150
																155
																160
gtt gtt tta tac atg gac cca atg tgc gat gcg ttc cca aaa tta															528	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
																165
																170
																175
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac															576	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
																180
																185
																190
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc															624	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
																195
																200
																205
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt															672	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
																210
																215
																220
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc															720	
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	
																225
																230
																235
																240
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt															768	
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	
																245
																250
																255
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act															816	
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	
																260
																265
																270
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc															864	
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	
																275
																280
																285
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt															912	
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	
																290
																295
																300
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca															960	
Glu	Arg	Phe	His	Ile	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	

305	310	315	320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 325		330		1008
			335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340		345		1056
			350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu His Ser Leu Gln Asp Leu Lys Ala 355		360		1104
			365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370		375		1152
			380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385		390		1200
			395	
			400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405		410		1248
			415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser 420		425		1296
			430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435		440		1344
			445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450		455		1392
			460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465		470		1440
			475	
			480	
gta cga tcg gcc tcg ggc gtc gtt cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485		490		1488
			495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500		505		1536
			510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr 515		520		1584
			525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly 530		535		1632
			540	

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga		1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg		
545	550	555
560		
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg		1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met		
565	570	575
gtc gga gac ccg gga cg aag tgg tcc caa cag tcc aag cag gta cga		1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg		
580	585	590
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg		1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly		
595	600	605
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag		1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys		
610	615	620
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat		1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp		
625	630	635
640		
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat		1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His		
645	650	655
660		
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg		2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly		
665	670	
675		
680		
685		
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg		2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu		
675	680	685
gtg cca gca gca tag		2079
Val Pro Ala Ala		
690		

<210> 19  
 <211> 692  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa  
 230-692. Translation of SEQ ID NO: 18.

<400> 19  
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 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
     35                          40                          45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
     50                          55                          60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
     65                          70                          75                          80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
     85                          90                          95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
     100                         105                         110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
     115                         120                         125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
     130                         135                         140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
     145                         150                         155                         160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
     165                         170                         175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
     180                         185                         190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
     195                         200                         205  
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
     210                         215                         220  
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly  
     225                         230                         235                         240  
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
     245                         250                         255  
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Lys Thr  
     260                         265                         270  
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
     275                         280                         285  
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
     290                         295                         300  
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
     305                         310                         315                         320  
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp  
     325                         330                         335  
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
     340                         345                         350  
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
     355                         360                         365  
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
     370                         375                         380  
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
     385                         390                         395                         400  
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
     405                         410                         415  
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
     420                         425                         430  
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
     435                         440                         445  
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
     450                         455                         460  
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
     465                         470                         475                         480  
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val

485	490	495
Ser Leu Pro Thr Thr Leu Tyr Pro Thr	Leu Thr Phe Ser Pro	Pro Pro Leu
500	505	510
Pro Ala Glu Lys Gln Ala Leu Ala	Glu Asn Ser Ile	Leu Gly Tyr Tyr
515	520	525
Ser Lys Ile Val Phe Val Trp Asp Lys	Pro Trp Trp Arg	Glu Gln Gly
530	535	540
Phe Ser Gly Val Leu Gln Ser Ser Cys	Asp Pro Ile Ser Phe	Ala Arg
545	550	555
Asp Thr Ser Ile Asp Val Asp Arg Gln	Trp Ser Ile Thr Cys	Phe Met
565	570	575
Val Gly Asp Pro Gly Arg Lys Trp Ser	Gln Gln Ser Lys	Gln Val Arg
580	585	590
Gln Lys Ser Val Trp Asp Gln Leu Arg	Ala Ala Tyr	Glu Asn Ala Gly
595	600	605
Ala Gln Val Pro Glu Pro Ala Asn Val	Leu Glu Ile	Glu Trp Ser Lys
610	615	620
Gln Gln Tyr Phe Gln Gly Ala Pro Ser	Ala Val Tyr	Gly Leu Asn Asp
625	630	635
Leu Ile Thr Leu Gly Ser Ala Leu Arg	Thr Pro Phe Lys	Ser Val His
645	650	655
Phe Val Gly Thr Glu Thr Ser Leu Val	Trp Lys Gly Tyr	Met Glu Gly
660	665	670
Ala Ile Arg Ser Gly Gln Arg Gly	Ala Ala Glu Val	Val Ala Ser Leu
675	680	685
Val Pro Ala Ala		
690		

<210> 20  
<211> 1464  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> sig\_peptide  
<222> (1)...(72)  
<223> Barley Alpha Amylase signal sequence

<221> misc\_feature  
<222> (73)...(1464)  
<223> K:trAPAOcDNA

<221> CDS  
<222> (1)...(1461)

<221> misc\_feature  
<222> (73)...(75)  
<223> Added lysine residue

<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize.

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Met Ala Asn Lys His Leu Ser Leu Ser	Leu Phe Leu Val Leu Leu Gly		
-20	-15	-10	
ctc tcc gcc tcc ctc gcc agc ggc aaa	gac aac gtt gcg gac gtg gta	96	
Leu Ser Ala Ser Leu Ala Ser Gly	Lys Asp Asn Val Ala Asp Val Val		
-5	1	5	
gtg gtg ggc gct ggc ttg agc ggt ttg	gag acg gca cgc aaa gtc cag	144	
Val Val Gly Ala Gly Leu Ser Gly	Leu Glu Thr Ala Arg Lys Val Gln		
10	15	20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt	gag gcg atg gat cgt gta ggg	192	
Ala Ala Gly Leu Ser Cys Leu Val Leu	Glu Ala Met Asp Arg Val Gly		
25	30	35	40
gga aag act ctg agc gta caa tcg ggt	ccc ggc agg acg act atc aac	240	
Gly Lys Thr Leu Ser Val Gln Ser Gly	Pro Gly Arg Thr Thr Ile Asn		
45	50	55	
gac ctc ggc gct gcg tgg atc aat gac	agc aac caa agc gaa gta tcc	288	
Asp Leu Gly Ala Ala Trp Ile Asn Asp	Ser Asn Gln Ser Glu Val Ser		
60	65	70	
aga ttg ttt gaa aga ttt cat ttg gag	ggc gag ctc cag agg acg act	336	
Arg Leu Phe Glu Arg Phe His Leu Glu	Gly Leu Gln Arg Thr Thr		
75	80	85	
gga aat tca atc cat caa gca caa	gac ggt aca acc act aca gct cct	384	
Gly Asn Ser Ile His Gln Ala Gln Asp	Gly Thr Thr Thr Ala Pro		
90	95	100	
tat ggt gac tcc ttg ctg agc gag gag	gtt gca agt gca ctt gcg gaa	432	
Tyr Gly Asp Ser Leu Leu Ser Glu Glu	Val Ala Ser Ala Leu Ala Glu		
105	110	115	120
ctc ctc ccc gta tgg tct cag ctg atc	gaa gag cat agc ctt caa gac	480	
Leu Leu Pro Val Trp Ser Gln Leu Ile	Glu His Ser Leu Gln Asp		
125	130	135	
ctc aag gcg agc cct cag gcg aag	cgg ctc gac agt gtg agc ttc gcg	528	
Leu Lys Ala Ser Pro Gln Ala Lys Arg	Leu Asp Ser Val Ser Phe Ala		
140	145	150	
cac tac tgt gag aag gaa cta aac	ttg cct gct gtt ctc ggc gta gca	576	
His Tyr Cys Glu Lys Glu Leu Asn Leu	Pro Ala Val Leu Gly Val Ala		
155	160	165	
aac cag atc aca cgc gct ctg ctc	ggt gtg gaa gcc cac gag atc agc	624	
Asn Gln Ile Thr Arg Ala Leu Leu	Gly Val Glu Ala His Glu Ile Ser		
170	175	180	
atg ctt ttt ctc acc gac tac atc	aag agt gcc acc ggt ctc agt aat	672	
Met Leu Phe Leu Thr Asp Tyr Ile	Lys Ser Ala Thr Gly Leu Ser Asn		
185	190	195	200
att ttc tcg gac aag aaa gac ggc	ggg cag tat atg cga tgc aaa aca	720	
Ile Phe Ser Asp Lys Lys Asp Gly	Gly Gln Tyr Met Arg Cys Lys Thr		

205	210	215	
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly			768
220	225	230	
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser			816
235	240	245	
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys			864
250	255	260	
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser			912
265	270	275	280
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu			960
285	290	295	
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg			1008
300	305	310	
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser			1056
315	320	325	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr			1104
330	335	340	
tgt ttc atg gtc gga gac ccg gga cg aag tgg tcc caa cag tcc aag Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			1152
345	350	355	360
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			1200
365	370	375	
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			1248
380	385	390	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			1296
395	400	405	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			1344
410	415	420	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			1392
425	430	435	440

atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg 1440  
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val  
445 450 455

gct agc ctg gtg cca gca gca tag 1464  
Ala Ser Leu Val Pro Ala Ala  
460

<210> 21  
<211> 487  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> SIGNAL  
<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha  
amylase signal sequence, for expression and  
secretion of the mature trAPAO in maize.

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
-20 -15 -10  
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
-5 1 5  
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
10 15 20  
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
25 30 35 40  
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
45 50 55  
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
60 65 70  
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
75 80 85  
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
90 95 100  
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
105 110 115 120  
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
125 130 135  
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
140 145 150  
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
155 160 165  
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
170 175 180  
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
185 190 195 200  
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
205 210 215  
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
220 225 230

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<210> 22
<211> 1803
<212> DNA
<213> Exophiala spinifera
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<220>  
<221> CDS  
<222> (1)...(1800)

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
          20           25           30

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aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct 144  
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
                  35                 40                 45

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gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc 192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
      50           55           60

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ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac		240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr		
65	70	75
		80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg		288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly		
85	90	95
ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg		336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val		
100	105	110
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc		384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala		
115	120	125
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg		432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc		480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
160		
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag ggc atg gat cgt gta		528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
165	170	175
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc		576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
180	185	190
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta		624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
195	200	205
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg		672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
210	215	220
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct		720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala		
225	230	235
240		
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg		768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		
245	250	255
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa		816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
260	265	270
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc		864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
275	280	285

gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	912
290 295 300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	960
305 310 315 320	
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	1008
325 330 335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	1056
340 345 350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	1104
355 360 365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	1152
370 375 380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtc ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	1200
385 390 395 400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	1248
405 410 415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	1296
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	1344
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	1392
450 455 460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	1440
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	1488
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	1536
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
515	520	525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
530	535	540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
545	550	555	560
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg			1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
565	570	575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
580	585	590	
gtg gct agc ctg gtg cca gca gca tag			1803
Val Ala Ser Leu Val Pro Ala Ala			
595	600		
<210> 23			
<211> 600			
<212> PRT			
<213> Exophiala spinifera			
<400> 23			
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1	5	10	15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val			
20	25	30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro			
35	40	45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys			
50	55	60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr			
65	70	75	80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly			
85	90	95	
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val			
100	105	110	
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala			
115	120	125	
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val			
130	135	140	
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
145	150	155	160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
165	170	175	
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
180	185	190	
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val			
195	200	205	
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr			

210	215	220
Thr	Gly Asn Ser Ile His Gln Ala Gln Asp	Gly Thr Thr Thr Thr Ala
225	230	235 240
Pro	Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
	245	250 255
Glu	Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	
	260	265 270
Asp	Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	
	275	280 285
Ala	His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
	290	295 300
Ala	Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	
305	310	315 320
Ser	Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
	325	330 335
Asn	Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
	340	345 350
Thr	Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
	355	360 365
Gly	Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
	370	375 380
Ser	Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385	390	395 400
Lys	Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
	405	410 415
Ser	Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
	420	425 430
Leu	Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
	435	440 445
Arg	Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
	450	455 460
Ser	Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465	470	475 480
Thr	Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
	485	490 495
Lys	Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
	500	505 510
Glu	Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
	515	520 525
Glu	Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
	530	535 540
Gly	Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545	550	555 560
Lys	Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
	565	570 575
Tyr	Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
	580	585 590
Val	Ala Ser Leu Val Pro Ala Ala	
	595	600

<210> 24  
 <211> 3003  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Sequence is a barley alpha amylase signal  
 sequence: esp1 mat: an artificial spacer sequence  
 and K:trAPAO

<221> sig\_peptide  
 <222> (1)...(72)  
 <223> Barley alpha amylase signal sequence

<221> misc\_feature  
 <222> (73)...(1575)  
 <223> esp1 mat

<221> misc\_feature  
 <222> (1576)...(1611)  
 <223> spacer sequence

<221> misc\_feature  
 <222> (1612)...(3000)  
 <223> K:trAPAO

<221> CDS  
 <222> (1)...(3000)

<221> misc\_feature  
 <222> (1612)...(1614)  
 <223> Extra lysine

<400> 24

atg	gcc	aac	aag	cac	ctg	agc	ctc	tcc	ctc	ttc	ctc	gtg	ctc	ctc	ggc		48
Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly		
																-10	
ctc	tcc	gcc	tcc	ctc	gcc	agc	ggc	gct	cct	act	gtc	aag	att	gat	gct		96
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala		
																-5	
																1	
ggg	atg	gtg	gtc	ggc	acg	act	act	act	gtc	ccc	ggc	acc	act	gcg	acc		144
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr			
																10	
																15	
gtc	agc	gag	ttc	ttg	ggc	gtt	cct	ttt	gcc	gcc	tct	ccg	aca	cga	ttt		192
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe		
																25	
																30	
gct	cct	cct	act	cgt	ccc	gtg	cct	tgg	tca	acg	cct	ttg	caa	gcc	act		240
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr		
																45	
																50	
gca	tat	ggt	cca	gca	tgc	cct	caa	caa	ttc	aat	tac	ccc	gaa	gaa	ctc		288
Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu		
																60	
																65	
cgt	gag	att	acg	atg	gcc	tgg	ttc	aat	aca	ccg	ccc	ccg	tca	gct	ggt		336
Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Pro	Ser	Ala	Gly	
																75	
																80	
																85	

gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag		384	
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu			
90	95	100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa		432	
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu			
105	110	115	120
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc		480	
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala			
125	130	135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg		528	
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu			
140	145	150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg		576	
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly			
155	160	165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca		624	
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala			
170	175	180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg		672	
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala			
185	190	195	200
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca		720	
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro			
205	210	215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc		768	
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe			
220	225	230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc		816	
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu			
235	240	245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat		864	
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp			
250	255	260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag		912	
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu			
265	270	275	280
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc		960	
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg			
285	290	295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc		1008	
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala			
300	305	310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat		1056	

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr			
315	320	325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt		1104	
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
330	335	340	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag		1152	
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
345	350	355	360
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc		1200	
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
365	370	375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac		1248	
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
380	385	390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg		1296	
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
395	400	405	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca		1344	
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
410	415	420	
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc		1392	
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
425	430	435	440
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa		1440	
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
445	450	455	
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt		1488	
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
460	465	470	
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt		1536	
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
475	480	485	
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc		1584	
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
490	495	500	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg		1632	
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
505	510	515	520
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc		1680	
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
525	530	535	
cag gcc gcc ggt ctg tcc tgc gtt ctt gag gcg atg gat cgt gta		1728	
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			

540	545	550	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555	560	565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570	575	580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585	590	595	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 605	610	615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620	625	630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635	640	645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650	655	660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665	670	675	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685	690	695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700	705	710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715	720	725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730	735	740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745	750	755	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765	770	775	2400

aag gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790	2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805	2496
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 810 815 820	2544
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 825 830 835 840	2592
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 845 850 855	2640
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 860 865 870	2688
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 875 880 885	2736
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 890 895 900	2784
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 905 910 915 920	2832
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 925 930 935	2880
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 940 945 950	2928
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 955 960 965	2976
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 970 975	3003

<210> 25  
<211> 1000  
<212> PRT

<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1)...(24)

<223> translation of the BAA:ESP1:K:trAPAO construct  
sequence of SEQ ID NO: 24

<400> 25  
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-20 -15 -10  
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala  
-5 1 5  
Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr  
10 15 20  
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
25 30 35 40  
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr  
45 50 55  
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu  
60 65 70  
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly  
75 80 85  
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu  
90 95 100  
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu  
105 110 115 120  
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala  
125 130 135  
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu  
140 145 150  
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly  
155 160 165  
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala  
170 175 180  
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala  
185 190 195 200  
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro  
205 210 215  
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe  
220 225 230  
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu  
235 240 245  
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp  
250 255 260  
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu  
265 270 275 280  
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg  
285 290 295  
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala  
300 305 310  
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr  
315 320 325  
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu  
330 335 340  
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln

345	350	355	360
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
365	370	375	
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
380	385	390	
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
395	400	405	
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
410	415	420	
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
425	430	435	440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
445	450	455	
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
460	465	470	
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
475	480	485	
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
490	495	500	
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
505	510	515	520
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
525	530	535	
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
540	545	550	
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
555	560	565	
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val			
570	575	580	
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr			
585	590	595	600
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala			
605	610	615	
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
620	625	630	
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
635	640	645	
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
650	655	660	
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
665	670	675	680
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
685	690	695	
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
700	705	710	
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
715	720	725	
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
730	735	740	
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
745	750	755	760
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
765	770	775	
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
780	785	790	
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
795	800	805	

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
 810 815 820  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 825 830 835 840  
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
 845 850 855  
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
 860 865 870  
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 875 880 885  
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 890 895 900  
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 905 910 915 920  
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 925 930 935  
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 940 945 950  
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 955 960 965  
 Val Ala Ser Leu Val Pro Ala Ala  
 970 975

<210> 26  
 <211> 2976  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Barley alpha amylase signal sequence: BEST1  
 mature: artificial spacer: and K:trAPAO. For  
 plant expression.

<221> sig\_peptide  
 <222> (1)...(72)  
 <223> Barley alpha amylase signal sequence

<221> mat\_peptide  
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 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
     -20                       -15                       -10  
  
 ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc 96  
 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr  
     -5                       1                           5  
  
 gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144  
 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg  
   10                       15                           20  
  
 gga ata ccc tat gca gcg ccg cgt gtt ctg cgt tgg aag ccg 192  
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Leu Arg Trp Lys Pro  
   25                       30                           40  
  
 ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt 240  
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe  
   45                       50                           55  
  
 ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc 288  
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala  
   60                       65                           70  
  
 ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca 336  
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser  
   75                       80                           85  
  
 ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc 384  
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly  
   90                       95                           100  
  
 ggc ttc gcc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg 432  
 Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala  
   105                       110                           120  
  
 ctt gcg cga cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac 480  
 Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn  
   125                       130                           135  
  
 atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc 528  
 Ile Leu Gly Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
   140                       145                           150  
  
 gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg 576  
 Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
   155                       160                           165  
  
 tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg 624  
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
   170                       175                           180  
  
 acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc 672  
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
   185                       190                           195                       200

acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt		720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser		
205	210	215
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg		768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser		
220	225	230
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca		816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro		
235	240	245
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac		864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp		
250	255	260
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg		912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu		
265	270	275
280		
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt		960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Gly Gln Leu Ala Pro Val		
285	290	295
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg		1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly		
300	305	310
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg		1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala		
315	320	325
cag ttt ggc gac caa gcc gcc gtc gtg gcg gcg tgc tat ccc ctc gac		1104
Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp		
330	335	340
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat		1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn		
345	350	355
360		
cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag		1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln		
365	370	375
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga		1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly		
380	385	390
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg		1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val		
395	400	405
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc		1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro		
410	415	420

acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc		1392	
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val			
425	430	440	
cggttcgccaaatggc gaccccggggacgcccttacc tgg cct		1440	
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro			
445	450	455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc		1488	
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg			
460	465	470	
gcccgtgtgtcgcccggaccttccatccccttgcgcatggc		1536	
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly			
475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc		1584	
Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser			
490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtc gct ggc ttg agc ggt		1632	
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly			
505	510	515	520
ttttagacgcacca cgc aaa gtc cag gcc ggt ctg tcc tgc ctc gtt		1680	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			
525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg		1728	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
540	545	550	
ggcccccaggacactatcAACGACTCTGGC GCT GCG TGG ATC AAT		1776	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
555	560	565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg		1824	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
570	575	580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa		1872	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
585	590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag		1920	
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg		1968	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
620	625	630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag		2016	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
635	640	645	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac		2064	

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn		
650	655	660
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctc		2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu		
665	670	675
680		
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc		2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile		
685	690	695
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc		2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly		
700	705	710
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc		2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala		
715	720	725
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc		2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val		
730	735	740
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg		2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser		
745	750	755
760		
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc		2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr		
765	770	775
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa		2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln		
780	785	790
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
795	800	805
805		
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
810	815	820
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac		2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
825	830	835
840		
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
845	850	855
855		
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
860	865	870
870		
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890	880	885	2784
		895	900
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 905	910	915	2832
			920
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 925	930	935	2880
			935
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 940	945	950	2928
			950
caa cga ggt gct gca gaa gtt gtc gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 955	960	965	2973
			965
tag			2976
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<212> PRT			
<213> Artificial Sequence			
<220>			
<221> SIGNAL			
<222> (1)...(24)			
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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr -5 1 5			
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg 10 15 20			
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro 25 30 35 40			
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe 45 50 55			
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala 60 65 70			
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser 75 80 85			
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly 90 95 100			
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala 105 110 115 120			
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125 130 135			

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
     140                  145                  150  
 Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
     155                  160                  165  
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
     170                  175                  180  
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
     185                  190                  195                  200  
 Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser  
     205                  210                  215  
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser  
     220                  225                  230  
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro  
     235                  240                  245  
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp  
     250                  255                  260  
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu  
     265                  270                  275                  280  
 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val  
     285                  290                  295  
 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly  
     300                  305                  310  
 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala  
     315                  320                  325  
 Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp  
     330                  335                  340  
 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn  
     345                  350                  355                  360  
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln  
     365                  370                  375  
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly  
     380                  385                  390  
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val  
     395                  400                  405  
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro  
     410                  415                  420  
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val  
     425                  430                  435                  440  
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro  
     445                  450                  455  
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg  
     460                  465                  470  
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly  
     475                  480                  485  
 Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
     490                  495                  500  
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly  
     505                  510                  515                  520  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
     525                  530                  535  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
     540                  545                  550  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
     555                  560                  565  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
     570                  575                  580  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln

585	590	595	600												
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
					605			610						615	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
					620			625						630	
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
					635			640						645	
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
					650			655						660	
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
					665			670						680	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
					685			690						695	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
					700			705						710	
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
					715			720						725	
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
					730			735						740	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
					745			750						760	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
					765			770						775	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
					780			785						790	
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
					795			800						805	
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
					810			815						820	
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
					825			830						840	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
					845			850						855	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
					860			865						870	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
					875			880						885	
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
					890			895						900	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
					905			910						920	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
					925			930						935	
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
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Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
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<211> 3618  
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<220>  
<223> gst:espl:sp:K:trAPAO. For bacterial expression.

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<221> CDS
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<221> misc_feature
<222> (1)....(687)
<223> gast + polylinker

<221> mat_peptide
<222> (688)....(2190)
<223> esp1 mat

<221> misc_feature
<222> (2191)....(2226)
<223> spacer sequence

<221> misc_feature
<222> (2227)....(3615)
<223> K:trAPAO

<221> misc_feature
<222> (2227)....(2229)
<223> Extra lysine

<400> 28
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc      48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1           5           10          15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20          25          30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg     144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35          40          45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa     192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50          55          60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac     240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65          70          75          80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa     288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85          90          95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt     336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100          105         110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa     384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115          120         125

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atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat		432	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
130	135	140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat		480	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
145	150	155	160
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta		528	
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
165	170	175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac		576	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc		624	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt		672	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg		720	
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val			
225	230	235	240
gtc ggc acg act act gtc ccc ggc acc act gcg acc gtc agc gag		768	
Val Gly Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu			
245	250	255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct		816	
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro			
260	265	270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt		864	
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly			
275	280	285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att		912	
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile			
290	295	300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag		960	
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu			
305	310	315	320
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac		1008	
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn			
325	330	335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg		1056	
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp			
340	345	350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat		1104	

Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp			
355	360	365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro			1152
370	375	380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp			1200
385	390	395	400
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly			1248
405	410	415	
ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg			1296
420	425	430	
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg			1344
435	440	445	
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly			1392
450	455	460	
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr			1440
465	470	475	480
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr			1488
485	490	495	
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu			1536
500	505	510	
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly			1584
515	520	525	
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly			1632
530	535	540	
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu			1680
545	550	555	560
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr			1728
565	570	575	
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala			1776

580	585	590	
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595	600	605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610	615	620	1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625	630	635	1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645	650	655	1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660	665	670	2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675	680	685	2064
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690	695	700	2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705	710	715	2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly 725	730	735	2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740	745	750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755	760	765	2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770	775	780	2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785	790	795	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805	810	815	2448

ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn	2496
820	825
	830
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly	2544
835	840
	845
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu	2592
850	855
	860
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys	2640
865	870
	875
	880
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr	2688
885	890
	895
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln	2736
900	905
	910
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	2784
915	920
	925
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	2832
930	935
	940
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met	2880
945	950
	955
	960
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	2928
965	970
	975
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	2976
980	985
	990
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val	3024
995	1000
	1005
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro	3072
1010	1015
	1020
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr	3120
1025	1030
	1035
	1040

tat	aag	ata	gtc	tgc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	3168	
Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	
1045															1055	
ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	3216
Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	
1060															1070	
aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	3264
Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	
1075															1085	
atg	gtc	gga	gac	ccg	gga	cg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	3312
Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	
1090															1100	
cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cg	gca	gcc	tac	gag	aac	gcc	3360
Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	
1105															1120	
ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	3408
Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	
1125															1135	
aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	3456
Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	
1140															1150	
gat	ctc	atc	aca	ctg	ggt	tcg	g	ctc	aga	acg	ccg	ttc	aag	agt	gtt	3504
Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	
1155															1165	
cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	3552
His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	
1170															1180	
ggg	gcc	ata	cga	tcg	ggt	caa	cga	ggt	gct	gca	gaa	gtt	gtg	gct	agc	3600
Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	
1185															1200	
ctg	gtg	cca	gca	gca	tag										3618	
Leu	Val	Pro	Ala	Ala												
					1205											

<210> 29  
<211> 1205  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Translation of the GST:ESP1:K:trAPAO fusion  
sequence for bacterial expression as provided in  
SEQ ID NO: 28

<400> 29  
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1	5	10	15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20	25	30	
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
35	40	45	
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
50	55	60	
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
65	70	75	80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
85	90	95	
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
100	105	110	
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
115	120	125	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
130	135	140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
145	150	155	160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
165	170	175	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val			
225	230	235	240
Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu			
245	250	255	
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro			
260	265	270	
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly			
275	280	285	
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile			
290	295	300	
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu			
305	310	315	320
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn			
325	330	335	
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp			
340	345	350	
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp			
355	360	365	
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro			
370	375	380	
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp			
385	390	395	400
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly			
405	410	415	
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg			
420	425	430	
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg			
435	440	445	
Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly			
450	455	460	

Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr  
 465 470 475 480  
 Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr  
 485 490 495  
 Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu  
 500 505 510  
 Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly  
 515 520 525  
 Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly  
 530 535 540  
 Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu  
 545 550 555 560  
 Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr  
 565 570 575  
 Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala  
 580 585 590  
 Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln  
 595 600 605  
 Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala  
 610 615 620  
 Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser  
 625 630 635 640  
 Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr  
 645 650 655  
 Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala  
 660 665 670  
 Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn  
 675 680 685  
 Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser  
 690 695 700  
 Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr  
 705 710 715 720  
 Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly  
 725 730 735  
 Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val  
 740 745 750  
 Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala  
 755 760 765  
 Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys  
 770 775 780  
 Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu  
 785 790 795 800  
 Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu  
 805 810 815  
 Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn  
 820 825 830  
 Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly  
 835 840 845  
 Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu  
 850 855 860  
 Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys  
 865 870 875 880  
 Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr  
 885 890 895  
 Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln  
 900 905 910  
 Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu

915	920	925
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe		
930	935	940
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met		
945	950	955
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val		
965	970	975
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys		
980	985	990
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val		
995	1000	1005
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro		
1010	1015	1020
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr		
1025	1030	1035
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln		
1045	1050	1055
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala		
1060	1065	1070
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe		
1075	1080	1085
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val		
1090	1095	1100
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala		
1105	1110	1115
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser		
1125	1130	1135
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn		
1140	1145	1150
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val		
1155	1160	1165
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu		
1170	1175	1180
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser		
1185	1190	1195
Leu Val Pro Ala Ala		
1205		

<210> 30  
<211> 3591  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Nucleotide sequence for a GST:BEST1:K:trAPAO fusion for bacterial expression in a pGEX-4T-1 or similar vector

<221> misc\_feature  
<222> (1)...(687)  
<223> gst + polylinker  
  
<221> mat\_peptide  
<222> (688)...(2163)  
<223> BEST1 mature

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<221> misc_feature
<222> (2164)...(2199)
<223> spacer sequence

<221> misc_feature
<222> (2200)...(3588)
<223> K:trAPAO

<221> CDS
<222> (1)...(3588)

<221> misc_feature
<222> (2200)...(2202)
<223> Extra lysine

<400> 30
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc      48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1           5           10          15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20          25          30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg     144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35          40          45

ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa     192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50          55          60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac     240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65          70          75          80

atg ttg ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa     288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85          90          95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt     336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100          105         110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa     384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115          120          125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat     432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130          135          140

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat     480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145          150          155          160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta     528

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Val Val Leu Tyr Met Asp Pro Met Cys	Leu Asp Ala Phe Pro Lys Leu	
165	170	175
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac		576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr		
180	185	190
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc		624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala		
195	200	205
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt		672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg		
210	215	220
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc		720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly		
225	230	235
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc		768
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro		
245	250	255
tat gca gcg ccg cct gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac		816
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His		
260	265	270
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac		864
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp		
275	280	285
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg		912
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val		
290	295	300
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa		960
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys		
305	310	315
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac gcc ggc ggc ttc gcc		1008
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala		
325	330	335
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga		1056
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg		
340	345	350
cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac atc ctg ggc		1104
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly		
355	360	365
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg		1152
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser		
370	375	380
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag		1200
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln		

385	390	395	400	
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe 405 410 415				1248
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro 420 425 430				1296
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu 435 440 445				1344
acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg 450 455 460				1392
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu 465 470 475 480				1440
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg 485 490 495				1488
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr 500 505 510				1536
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cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag ggc gcg ccc Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro 595 600 605				1824
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gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu 625	630	635	640	1920
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala 645	650	655		1968
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala 660	665	670		2016
aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser 675	680	685		2064
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gcg gtg Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val 690	695	700		2112
gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala 705	710	715	720	2160
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn 725	730	735		2208
gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr 740	745	750		2256
gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt ctt gag gcg Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala 755	760	765		2304
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly 770	775	780		2352
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn 785	790	795	800	2400
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu 805	810	815		2448
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr 820	825	830		2496
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala 835	840	845		2544

agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag		2592	
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu			
850	855	860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac		2640	
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp			
865	870	875	880
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct		2688	
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala			
885	890	895	
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Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu			
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Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala			
915	920	925	
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Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr			
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atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag		2880	
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys			
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gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att		2928	
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile			
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Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val			
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Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro			
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Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala			
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gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac		3120	
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp			
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Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser			
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tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga		3216	
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg			
1060	1065	1070	
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga aag tgg		3264	

Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp			
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tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc			3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu			
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cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac			3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn			
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Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro			
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agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc			3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu			
1140	1145	1150	
aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta			3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu			
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Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly			
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
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Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
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 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
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 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
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 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
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 Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly  
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 Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro  
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 Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly  
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 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser  
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 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln  
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Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn		
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Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro		
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Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu		
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Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala		
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Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala		
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Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser		
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Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val		
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Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala		
705	710	715
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn		
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Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr		
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Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala		
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Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu		
850	855	860
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp		
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Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala		
885	890	895
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu		
900	905	910
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala		
915	920	925
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr		
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Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys		
945	950	955
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile		
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Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val		
980	985	990
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro		
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Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala		
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 Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser  
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 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg  
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 Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp  
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 Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu  
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 1105 1110 1115 1120  
 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro  
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 Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu  
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 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu  
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Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
 gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
 ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
 acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
 gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca	720
Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro	
225 230 235 240	
 aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac	768

Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp			
245	250	255	
gga ggg agg tat gtg aca ata gct gga cag att gga caa gac gct tcg	816		
Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser			
260	265	270	
ggc gtg aca gac cct gcc tac gag aaa cag gtt gcc caa gca ttc gcc	864		
Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala			
275	280	285	
aat ctg cga gct tgc ctt gct gca gtt gga gcc act tca aac gac gtc	912		
Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val			
290	295	300	
acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc	960		
Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr			
305	310	315	320
gca att gga gat ggg ctg aag gct acc ttt gcc ctt gac agg ctc cct	1008		
Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro			
325	330	335	
cct tgc acg ctg gtg cca gtg tcg gcc ttg tct tca cct gaa tac ctc	1056		
Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu			
340	345	350	
ttt gag gtt gat gcc acg gcg ctg gtg ccg gga cac acg acc cca gac	1104		
Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp			
355	360	365	
aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag	1152		
Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu			
370	375	380	
acg gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt ctt gag	1200		
Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu			
385	390	395	400
gcf atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc	1248		
Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro			
405	410	415	
ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc tcc gac agc	1296		
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser			
420	425	430	
aac caa aac gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc	1344		
Asn Gln Asn Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly			
435	440	445	
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt	1392		
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly			
450	455	460	
aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt	1440		
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val			

465	470	475	480	
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu 485 490 495				1488
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cg <sup>g</sup> ctc Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu 500 505 510				1536
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct Asp Ser Val Ser Phe Ala His Tyr Cys Glu Leu Asn Leu Pro 515 520 525				1584
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val 530 535 540				1632
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser 545 550 555 560				1680
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln 565 570 575				1728
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser 580 585 590				1776
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu 595 600 605				1824
att gag cag tcg gca tcc ggc tgg aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 610 615 620				1872
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr 625 630 635 640				1920
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 645 650 655				1968
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp 660 665 670				2016
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser 675 680 685				2064
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp 690 695 700				2112

cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag		2160
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys		
705	710	715
		720
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa		2208
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln		
725	730	735
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc		2256
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala		
740	745	750
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct		2304
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala		
755	760	765
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg		2352
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala		
770	775	780
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct		2400
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser		
785	790	795
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga		2448
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg		
805	810	815
ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag		2490
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
820	825	

<210> 33  
<211> 829  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Translation of SEQ ID NO: 32 showing sequence of GST:APAO in which 2 APAO amino acids have been changed by site-directed mutagenesis to eliminate 2 potential glycosylation sites

<400> 33  
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1               5               10               15  
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20              25              30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35              40              45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50              55              60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65              70              75              80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu

	85	90	95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
100	105	110	
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
115	120	125	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
130	135	140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
145	150	155	160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
165	170	175	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro			
225	230	235	240
Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp			
245	250	255	
Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser			
260	265	270	
Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala			
275	280	285	
Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val			
290	295	300	
Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr			
305	310	315	320
Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro			
325	330	335	
Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu			
340	345	350	
Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp			
355	360	365	
Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu			
370	375	380	
Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu			
385	390	395	400
Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro			
405	410	415	
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser			
420	425	430	
Asn Gln Asn Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly			
435	440	445	
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly			
450	455	460	
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val			
465	470	475	480
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu			
485	490	495	
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu			
500	505	510	
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro			
515	520	525	
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val			
530	535	540	

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser  
 545 550 555 560  
 Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln  
 565 570 575  
 Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser  
 580 585 590  
 Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu  
 595 600 605  
 Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala  
 610 615 620  
 Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr  
 625 630 635 640  
 Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu  
 645 650 655  
 Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp  
 660 665 670  
 Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser  
 675 680 685  
 Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp  
 690 695 700  
 Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys  
 705 710 715 720  
 Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln  
 725 730 735  
 Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala  
 740 745 750  
 Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala  
 755 760 765  
 Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala  
 770 775 780  
 Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser  
 785 790 795 800  
 Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
 805 810 815  
 Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 820 825

<210> 34  
 <211> 11  
 <212> PRT  
 <213> Exophiala spinifera

<220>  
 <221> BINDING  
 <222> (0)...(0)  
 <223> Amino-terminal dinucleotide (ADP) binding region  
     of trAPAO amino oxidase domain, characterized by a  
     beta-alpha-beta stretch containing 3 invariant  
     glycines (GXGXXG) in the beta-alpha turn.

<400> 34  
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10

<210> 35

<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Example spacer sequence

<400> 35  
Gly Gly Gly Ser Gly Gly Gly Ser  
1 5